



PCT

RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/505,263

TIME: 15:58:27

Input Set : D:\1242-50-2-PCT-US.ST25.txt

Output Set: N:\CRF4\08262004\J505263.raw

3 <110> APPLICANT: Vanderbilt University
 4 Case Western Reserve University
 5 The Brigham and Women's Hospital, Inc.
 6 Mount, David B
 7 Romero, Michael
 9 <120> TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and
 SLC26A2
 10 ANION EXCHANGERS
 12 <130> FILE REFERENCE: 1242/50/2 PCT/US
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/505,263
 C--> 14 <141> CURRENT FILING DATE: 2004-08-20
 14 <150> PRIOR APPLICATION NUMBER: US 60/360,275
 15 <151> PRIOR FILING DATE: 2002-02-28
 17 <150> PRIOR APPLICATION NUMBER: PCT/US03/06469
 18 <151> PRIOR FILING DATE: 2003-02-28
 20 <160> NUMBER OF SEQ ID NOS: 96
 22 <170> SOFTWARE: PatentIn version 3.2
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2654
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
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 34 aatggacctg cggaggcgag actaccacat ggaacggccg ctgctgaacc aggagcattt 180
 36 ggaggagctg gggcgctggg gctcagcacc taggaccac cagtggcgga cctgggttga 240
 38 gtgctcccg tgcgggct atgcccttct gctccaacac ctcccggttt tgggtctggt 300
 40 accccggtat cctgtgcgtg actggctcct ggggtgacctg ttatccggcc tgagtgtggc 360
 42 catcatgcag cttccgcagg gcttggccta cgccctcctg gctggattgc ccccgtgtt 420
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 46 catctccgtg gggacctttg ctgtcatgtc tgtgatggtg ggcagtgtga cagaatccct 540
 48 ggccccgcag gccttgaacg actccatgat caatgagaca gccagagatg ctgcccgggt 600
 50 acaggtggcc tccacactca gtgtcctggt tggcctcttc caggtggggc tgggcctgat 660
 52 ccacttcggc ttcgtggtea cctacctgtc agaacctctt gtccgaggct ataccacagc 720
 54 tgcagctgtg caggtcttcg tctcacagct caagtatgtg tttggcctcc atctgagcag 780
 56 ccactctggg ccactgtccc tcatctatac agtgetggag gtctgctgga agctgcccc 840
 58 gagcaagggt ggcaccgtgg tcaactgcagc tgtggctggg gtggtgctcg tgggtggtgaa 900
 60 gctgttgaat gacaagctgc agcagcagct gcccatgccg ataccggggg agctgctcac 960
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 64 tgtcgtgggc aacatccctg cagggtcgtt gccccagtg gcccccaaca cccagctgtt 1080
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78 cgacatgcgc tccctctgga aggccaatcg ggcggatctg cttatctggc tggtagacctt 1500
80 cacggccacc atcttgetga acctggacct tggcttggtg gttgcgggtca tcttctccct 1560
82 gctgctcgtg gtggtccgga cacagatgcc ccactactct gtcttggggc aggtgccaga 1620
84 caggatatt tacagagatg tggcagagta ctcagaggcc aagggaagtcc ggggggtgaa 1680
86 ggtcttccgc tcctcggcca ccgtgtactt tgccaatgct gagttctaca gtgatgcgct 1740
88 gaagcagagg tgtggtgtgg atgtcgactt cctcatctcc cagaagaaga aactgctcaa 1800
90 gaagcaggag cagctgaagc tgaagcaact gcagaaagag gagaagcttc ggaaacaggc 1860
92 tgcttcccc aagggcgcct cagtttccat taatgtcaac accagccttg aagacatgag 1920
94 gagcaacaac gttgaggact gcaagatgat ggtgagctca ggagataaga tggagatgc 1980
96 aacagccaat ggtcaagaag actccaaggc cccagatggg tccacactga aggccttggg 2040
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100 cactgtgtgc ctcaagagcc tgaagaatat ttccatgac ttccgggaga ttgaggtgga 2160
102 ggtgtacatg ggcgcctgcc acagcctgt ggtcagccag cttgaggctg ggcacttctt 2220
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112 ggaaggaggt cctgggactc caagttcagc gctccagggtc tgggacaggc cctgcatgca 2520
114 gtcaggctgg cagtggcgcg gtacaggag ggaactggtg catattttag cctcaggaat 2580
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128 Met Gly Leu Ala Asp Ala Ser Gly Pro Arg Asp Thr Gln Ala Leu Leu
129 1 5 10 15
132 Ser Ala Thr Gln Ala Met Asp Leu Arg Arg Arg Asp Tyr His Met Glu
133 20 25 30
136 Arg Pro Leu Leu Asn Gln Glu His Leu Glu Glu Leu Gly Arg Trp Gly
137 35 40 45
140 Ser Ala Pro Arg Thr His Gln Trp Arg Thr Trp Leu Gln Cys Ser Arg
141 50 55 60
144 Ala Arg Ala Tyr Ala Leu Leu Leu Gln His Leu Pro Val Leu Val Trp
145 65 70 75 80
148 Leu Pro Arg Tyr Pro Val Arg Asp Trp Leu Leu Gly Asp Leu Leu Ser
149 85 90 95
152 Gly Leu Ser Val Ala Ile Met Gln Leu Pro Gln Gly Leu Ala Tyr Ala
153 100 105 110
156 Leu Leu Ala Gly Leu Pro Pro Val Phe Gly Leu Tyr Ser Ser Phe Tyr
157 115 120 125
160 Pro Val Phe Ile Tyr Phe Leu Phe Gly Thr Ser Arg His Ile Ser Val
161 130 135 140
164 Gly Thr Phe Ala Val Met Ser Val Met Val Gly Ser Val Thr Glu Ser
165 145 150 155 160
168 Leu Ala Pro Gln Ala Leu Asn Asp Ser Met Ile Asn Glu Thr Ala Arg

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| | | | | | | |
|-----|---|-----|-----|-----|-----|-----|
| 169 | | 165 | | 170 | | 175 |
| 172 | Asp Ala Ala Arg Val Gln Val Ala Ser Thr Leu Ser Val Leu Val Gly | | | | | |
| 173 | | 180 | | 185 | | 190 |
| 176 | Leu Phe Gln Val Gly Leu Gly Leu Ile His Phe Gly Phe Val Val Thr | | | | | |
| 177 | | 195 | | 200 | | 205 |
| 180 | Tyr Leu Ser Glu Pro Leu Val Arg Gly Tyr Thr Thr Ala Ala Ala Val | | | | | |
| 181 | | 210 | | 215 | | 220 |
| 184 | Gln Val Phe Val Ser Gln Leu Lys Tyr Val Phe Gly Leu His Leu Ser | | | | | |
| 185 | 225 | | 230 | | 235 | 240 |
| 188 | Ser His Ser Gly Pro Leu Ser Leu Ile Tyr Thr Val Leu Glu Val Cys | | | | | |
| 189 | | 245 | | 250 | | 255 |
| 192 | Trp Lys Leu Pro Gln Ser Lys Val Gly Thr Val Val Thr Ala Ala Val | | | | | |
| 193 | | 260 | | 265 | | 270 |
| 196 | Ala Gly Val Val Leu Val Val Val Lys Leu Leu Asn Asp Lys Leu Gln | | | | | |
| 197 | | 275 | | 280 | | 285 |
| 200 | Gln Gln Leu Pro Met Pro Ile Pro Gly Glu Leu Leu Thr Leu Ile Gly | | | | | |
| 201 | | 290 | | 295 | | 300 |
| 204 | Ala Thr Gly Ile Ser Tyr Gly Met Gly Leu Lys His Arg Phe Glu Val | | | | | |
| 205 | 305 | | 310 | | 315 | 320 |
| 208 | Asp Val Val Gly Asn Ile Pro Ala Gly Leu Val Pro Pro Val Ala Pro | | | | | |
| 209 | | 325 | | 330 | | 335 |
| 212 | Asn Thr Gln Leu Phe Ser Lys Leu Val Gly Ser Ala Phe Thr Ile Ala | | | | | |
| 213 | | 340 | | 345 | | 350 |
| 216 | Val Val Gly Phe Ala Ile Ala Ile Ser Leu Gly Lys Ile Phe Ala Leu | | | | | |
| 217 | | 355 | | 360 | | 365 |
| 220 | Arg His Gly Tyr Arg Val Asp Ser Asn Gln Glu Leu Val Ala Leu Gly | | | | | |
| 221 | | 370 | | 375 | | 380 |
| 224 | Leu Ser Asn Leu Ile Gly Gly Ile Phe Gln Cys Phe Pro Val Ser Cys | | | | | |
| 225 | 385 | | 390 | | 395 | 400 |
| 228 | Ser Met Ser Arg Ser Leu Val Gln Glu Ser Thr Gly Gly Asn Ser Gln | | | | | |
| 229 | | 405 | | 410 | | 415 |
| 232 | Val Ala Gly Ala Ile Ser Ser Leu Phe Ile Leu Leu Ile Ile Val Lys | | | | | |
| 233 | | 420 | | 425 | | 430 |
| 236 | Leu Gly Glu Leu Phe His Asp Leu Pro Lys Ala Val Leu Ala Ala Ile | | | | | |
| 237 | | 435 | | 440 | | 445 |
| 240 | Ile Ile Val Asn Leu Lys Gly Met Leu Arg Gln Leu Ser Asp Met Arg | | | | | |
| 241 | | 450 | | 455 | | 460 |
| 244 | Ser Leu Trp Lys Ala Asn Arg Ala Asp Leu Leu Ile Trp Leu Val Thr | | | | | |
| 245 | 465 | | 470 | | 475 | 480 |
| 248 | Phe Thr Ala Thr Ile Leu Leu Asn Leu Asp Leu Gly Leu Val Val Ala | | | | | |
| 249 | | 485 | | 490 | | 495 |
| 252 | Val Ile Phe Ser Leu Leu Leu Val Val Val Arg Thr Gln Met Pro His | | | | | |
| 253 | | 500 | | 505 | | 510 |
| 256 | Tyr Ser Val Leu Gly Gln Val Pro Asp Thr Asp Ile Tyr Arg Asp Val | | | | | |
| 257 | | 515 | | 520 | | 525 |
| 260 | Ala Glu Tyr Ser Glu Ala Lys Glu Val Arg Gly Val Lys Val Phe Arg | | | | | |
| 261 | | 530 | | 535 | | 540 |
| 264 | Ser Ser Ala Thr Val Tyr Phe Ala Asn Ala Glu Phe Tyr Ser Asp Ala | | | | | |
| 265 | 545 | | 550 | | 555 | 560 |

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268 Leu Lys Gln Arg Cys Gly Val Asp Val Asp Phe Leu Ile Ser Gln Lys
269           565           570           575
272 Lys Lys Leu Leu Lys Lys Gln Glu Gln Leu Lys Leu Lys Gln Leu Gln
273           580           585           590
276 Lys Glu Glu Lys Leu Arg Lys Gln Ala Ala Ser Pro Lys Gly Ala Ser
277           595           600           605
280 Val Ser Ile Asn Val Asn Thr Ser Leu Glu Asp Met Arg Ser Asn Asn
281           610           615           620
284 Val Glu Asp Cys Lys Met Met Val Ser Ser Gly Asp Lys Met Glu Asp
285 625           630           635           640
288 Ala Thr Ala Asn Gly Gln Glu Asp Ser Lys Ala Pro Asp Gly Ser Thr
289           645           650           655
292 Leu Lys Ala Leu Gly Leu Pro Gln Pro Asp Phe His Ser Leu Ile Leu
293           660           665           670
296 Asp Leu Gly Ala Leu Ser Phe Val Asp Thr Val Cys Leu Lys Ser Leu
297           675           680           685
300 Lys Asn Ile Phe His Asp Phe Arg Glu Ile Glu Val Glu Val Tyr Met
301           690           695           700
304 Ala Ala Cys His Ser Pro Val Val Ser Gln Leu Glu Ala Gly His Phe
305 705           710           715           720
308 Phe Asp Ala Ser Ile Thr Lys Lys His Leu Phe Ala Ser Val His Asp
309           725           730           735
312 Ala Val Thr Phe Ala Leu Gln His Pro Arg Pro Val Pro Asp Ser Pro
313           740           745           750
316 Val Ser Val Thr Arg Leu
317           755
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321 <211> LENGTH: 2748
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323 <213> ORGANISM: Homo sapiens
326 <220> FEATURE:
327 <221> NAME/KEY: CDS
328 <222> LOCATION: (252)..(2468)
330 <400> SEQUENCE: 3
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333 gccacagat gccagctggg ggctggaata ctgtaccttg atcttagggc ctggaaaaat      120
335 caggtaggta actctctggt cctaggtgga ggtgtagggg aggttgggcc agggatgcct      180
337 tcaactgtgtc tctctggtct tgccacccca gaccgagggg cacacaggca ctgctgtctg      240
339 caacacaagc a atg gac ctg cgg agg cga gac tac cac atg gaa cgg ccg      290
340           Met Asp Leu Arg Arg Arg Asp Tyr His Met Glu Arg Pro
341           1           5           10
343 ctg ctg aac cag gag cat ttg gag gag ctg ggg cgc tgg ggc tca gca      338
344 Leu Leu Asn Gln Glu His Leu Glu Glu Leu Gly Arg Trp Gly Ser Ala
345 15           20           25
347 cct agg acc cac cag tgg cgg acc tgg ttg cag tgc tcc cgt gct cgg      386
348 Pro Arg Thr His Gln Trp Arg Thr Trp Leu Gln Cys Ser Arg Ala Arg
349 30           35           40           45
351 gcc tat gcc ctt ctg ctc caa cac ctc ccg gtt ttg gtc tgg tta ccc      434
352 Ala Tyr Ala Leu Leu Leu Gln His Leu Pro Val Leu Val Trp Leu Pro

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|-----|---|-----|-----|-----|-----|-----|------|
| 353 | | 50 | | 55 | | 60 | |
| 355 | cgg tat cct gtg cgt gac tgg ctc ctg ggt gac ctg tta tcc ggc ctg | | | | | | 482 |
| 356 | Arg Tyr Pro Val Arg Asp Trp Leu Leu Gly Asp Leu Leu Ser Gly Leu | | | | | | |
| 357 | | 65 | | 70 | | 75 | |
| 359 | agt gtg gcc atc atg cag ctt ccg cag ggc ttg gcc tac gcc ctc ctg | | | | | | 530 |
| 360 | Ser Val Ala Ile Met Gln Leu Pro Gln Gly Leu Ala Tyr Ala Leu Leu | | | | | | |
| 361 | | 80 | | 85 | | 90 | |
| 363 | gct gga ttg ccc ccc gtg ttt ggc ctc tat agc tcc ttc tac cct gtc | | | | | | 578 |
| 364 | Ala Gly Leu Pro Pro Val Phe Gly Leu Tyr Ser Ser Phe Tyr Pro Val | | | | | | |
| 365 | | 95 | | 100 | | 105 | |
| 367 | ttc atc tac ttc ctg ttt ggc act tcc cgg cac atc tcc gtg ggg acc | | | | | | 626 |
| 368 | Phe Ile Tyr Phe Leu Phe Gly Thr Ser Arg His Ile Ser Val Gly Thr | | | | | | |
| 369 | 110 | | 115 | | 120 | | 125 |
| 371 | ttt gct gtc atg tct gtg atg gtg ggc agt gtg aca gaa tcc ctg gcc | | | | | | 674 |
| 372 | Phe Ala Val Met Ser Val Met Val Gly Ser Val Thr Glu Ser Leu Ala | | | | | | |
| 373 | | 130 | | 135 | | 140 | |
| 375 | ccg cag gcc ttg aac gac tcc atg atc aat gag aca gcc aga gat gct | | | | | | 722 |
| 376 | Pro Gln Ala Leu Asn Asp Ser Met Ile Asn Glu Thr Ala Arg Asp Ala | | | | | | |
| 377 | | 145 | | 150 | | 155 | |
| 379 | gcc cgg gta cag gtg gcc tcc aca ctc agt gtc ctg gtt ggc ctc ttc | | | | | | 770 |
| 380 | Ala Arg Val Gln Val Ala Ser Thr Leu Ser Val Leu Val Gly Leu Phe | | | | | | |
| 381 | | 160 | | 165 | | 170 | |
| 383 | cag gtg ggg ctg ggc ctg atc cac ttc ggc ttc gtg gtc acc tac ctg | | | | | | 818 |
| 384 | Gln Val Gly Leu Gly Leu Ile His Phe Gly Phe Val Val Thr Tyr Leu | | | | | | |
| 385 | | 175 | | 180 | | 185 | |
| 387 | tca gaa cct ctt gtc cga ggc tat acc aca gct gca gct gtg cag gtc | | | | | | 866 |
| 388 | Ser Glu Pro Leu Val Arg Gly Tyr Thr Thr Ala Ala Ala Val Gln Val | | | | | | |
| 389 | 190 | | 195 | | 200 | | 205 |
| 391 | ttc gtc tca cag ctc aag tat gtg ttt ggc ctc cat ctg agc agc cac | | | | | | 914 |
| 392 | Phe Val Ser Gln Leu Lys Tyr Val Phe Gly Leu His Leu Ser Ser His | | | | | | |
| 393 | | 210 | | 215 | | 220 | |
| 395 | tct ggg cca ctg tcc ctc atc tat aca gtg ctg gag gtc tgc tgg aag | | | | | | 962 |
| 396 | Ser Gly Pro Leu Ser Leu Ile Tyr Thr Val Leu Glu Val Cys Trp Lys | | | | | | |
| 397 | | 225 | | 230 | | 235 | |
| 399 | ctg ccc cag agc aag gtt ggc acc gtg gtc act gca gct gtg gct ggg | | | | | | 1010 |
| 400 | Leu Pro Gln Ser Lys Val Gly Thr Val Val Thr Ala Ala Val Ala Gly | | | | | | |
| 401 | | 240 | | 245 | | 250 | |
| 403 | gtg gtg ctc gtg gtg gtg aag ctg ttg aat gac aag ctg cag cag cag | | | | | | 1058 |
| 404 | Val Val Leu Val Val Val Lys Leu Leu Asn Asp Lys Leu Gln Gln Gln | | | | | | |
| 405 | | 255 | | 260 | | 265 | |
| 407 | ctg ccc atg ccg ata ccc ggg gag ctg ctc acg ctc atc ggg gcc aca | | | | | | 1106 |
| 408 | Leu Pro Met Pro Ile Pro Gly Glu Leu Leu Thr Leu Ile Gly Ala Thr | | | | | | |
| 409 | 270 | | 275 | | 280 | | 285 |
| 411 | ggc atc tcc tat ggc atg ggt cta aag cac aga ttt gag gta gat gtc | | | | | | 1154 |
| 412 | Gly Ile Ser Tyr Gly Met Gly Leu Lys His Arg Phe Glu Val Asp Val | | | | | | |
| 413 | | 290 | | 295 | | 300 | |
| 415 | gtg ggc aac atc cct gca ggg ctg gtg ccc cca gtg gcc ccc aac acc | | | | | | 1202 |
| 416 | Val Gly Asn Ile Pro Ala Gly Leu Val Pro Pro Val Ala Pro Asn Thr | | | | | | |
| 417 | | 305 | | 310 | | 315 | |

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 2850

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2820